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and data reading device 50.

IN THE CLAIMS:

Please AMEND the claims as follow:

24. (TWICE AMENDED) [The]A method [according to claim 23.] for analyzing base sequence data and removing, based on said data, a vector base sequence from a recombinant DNA base sequence, comprising:

storing data identifying each of restriction enzymes and data of base sequences at a plurality of restriction enzyme sites of a plurality of vectors correspondingly, in a database;

searching base sequence data of a recombinant DNA obtained by splicing an object DNA fragment into a vector;

obtaining the base sequence data at a front restriction enzyme site and the base sequence data at a back restriction enzyme site, as specified by corresponding to a restriction enzyme used for cleaving the vector and a restriction enzyme used for obtaining the object DNA fragment, from the database;

generating a first forward retrieval key using the obtained base sequence data of the front restriction enzyme site and a first backward retrieval key using the obtained base sequence data of the back restriction enzyme site;

retrieving base sequence data of the recombinant DNA obtained by a search using the first forward and first backward retrieval keys, and specifying a junction between the vector and the object DNA fragment;

removing the vector base sequence at the specified junction,

wherein sequence data of the first forward retrieval key and of the first backward retrieval key are generated by base sequence data of the vector entered in a vector database, data of a multiple cloning site in the vector, and data of a restriction enzyme site in the multiple cloning site,

wherein data of a forward base sequence from a cleaving point in the restriction enzyme site in the multiple cloning site of the vector are acquired from the database, and a second forward retrieval key is generated using the acquired forward base sequence data of the cleaving point of the restriction enzyme site of the vector,

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performing first homology retrieval on condition that a first similarity value between retrieval base sequence data of the recombinant DNA and the first forward and first backward retrieval keys is equal to or larger than a predetermined value,

obtaining a candidate for a base sequence at the junction between the vector and the object DNA fragment according to a result of the first homology retrieval, and

performing a second homology retrieval on condition that a second similarity value between base sequence data of a plurality of first candidates for the junction, and base sequence data of the second forward retrieval key, is equal to or larger than a predetermined value.

25. (AS ONCE AMENDED) [The]A method [according to Claim 23,] for analyzing base sequence data and removing, based on said data, a vector base sequence from a recombinant DNA base sequence, comprising:

storing data identifying each of restriction enzymes and data of base sequences at a plurality of restriction enzyme sites of a plurality of vectors correspondingly, in a database;

searching base sequence data of a recombinant DNA obtained by splicing an object DNA fragment into a vector;

obtaining the base sequence data at a front restriction enzyme site and the base sequence data at a back restriction enzyme site, as specified by corresponding to a restriction enzyme used for cleaving the vector and a restriction enzyme used for obtaining the object DNA fragment, from the database;

generating a first forward retrieval key using the obtained base sequence data of the front restriction enzyme site and a first backward retrieval key using the obtained base sequence data of the back restriction enzyme site;

retrieving base sequence data of the recombinant DNA obtained by a search using the first forward and first backward retrieval keys, and specifying a junction between the vector and the object DNA fragment;

removing the vector base sequence at the specified junction,

wherein the sequence data of the first forward retrieval key and of the first backward retrieval key are generated by base sequence data of the vector entered in a

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vector database, data of a multiple cloning site in the vector, and data of a restriction enzyme site in the multiple cloning site,

wherein forward base sequence data of a forward cleaving point of the restriction enzyme site of the vector, and backward base sequence data of a backward cleaving point of the vector are acquired from the database, and a second forward retrieval key and a second backward retrieval key are generated using the base sequence data of the acquired forward and backward base sequence data of the cleaving points, respectively,

performing a first homology retrieval on condition that a first similarity value between retrieval base sequence data of the recombinant DNA and the first forward and first backward retrieval keys is equal to or larger than a predetermined value,

obtaining a candidate for a base sequence at the junction between the vector and the object DNA fragment according to a result of the first homology retrieval, and

performing a second homology retrieval on condition that a second similarity value between base sequence data of a plurality of first candidates for the junction, and base sequence data of the second forward retrieval key, is equal to or larger than a predetermined value.

26. (AS ONCE AMENDED) The method according to Claim 25, wherein the sequence data of the first forward and first backward retrieval keys are generated by base sequence data of the vector entered in a vector database, data of a multiple cloning site in the vector, and data of a restriction enzyme site in the multiple cloning site, and

wherein the second homology retrieval is performed using both the second forward and second backward retrieval keys.

28. (TWICE AMENDED) [The]A method [according to Claim 23,] for analyzing base sequence data and removing, based on said data, a vector base sequence from a recombinant DNA base sequence, comprising:

storing data identifying each of restriction enzymes and data of base sequences at a plurality of restriction enzyme sites of a plurality of vectors correspondingly, in a database;

searching base sequence data of a recombinant DNA obtained by

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splicing an object DNA fragment into a vector;

obtaining the base sequence data at a front restriction enzyme site and the base sequence data at a back restriction enzyme site, as specified by corresponding to a restriction enzyme used for cleaving the vector and a restriction enzyme used for obtaining the object DNA fragment, from the database;

generating a first forward retrieval key using the obtained base sequence data of the front restriction enzyme site and a first backward retrieval key using the obtained base sequence data of the back restriction enzyme site;

retrieving base sequence data of the recombinant DNA obtained by a search using the first forward and first backward retrieval keys, and specifying a junction between the vector and the object DNA fragment;

removing the vector base sequence at the specified junction,

wherein backward base sequence data from a cleaving point in a multiple cloning site of the vector corresponding to the restriction enzyme are acquired from the database, and a second backward retrieval key is generated using the acquired backward base sequence data of the cleaving point, [and] - - -

performing a first homology retrieval on condition that a first similarity value between retrieval base sequence data of the recombinant DNA and the first forward and first backward retrieval keys is equal to or larger than a predetermined value;

obtaining a first candidate for a base sequence at a junction between the vector and the object DNA fragment according to a result of the first homology retrieval; and

performing a second homology retrieval to identify at least one area in the vector on condition that a second similarity value between base sequence data of a first candidate for the junction, screened by using the first retrieval keys, and base sequence data of the second backward retrieval key is equal to or larger than a predetermined value.

29. (TWICE AMENDED) The method according to Claim 28,

wherein said [nucleic acid molecules of said] vector base sequence [are] is removed[from the recombinant DNA sequence data], when [the] only one area is specified by the second homology retrieval [is one].

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30. (AS ONCE AMENDED) The method according to Claim 25, further comprising:

obtaining, as a forward vector unit candidate for the vector base sequence, a forward base sequence selected by the second homology retrieval, and a base sequence before said forward base sequence; and

obtaining, as a backward vector unit candidate for the vector base sequence, a backward base sequence selected by the second homology retrieval, and a base sequence after said backward base sequence.

31. (TWICE AMENDED) The method according to Claim [29]30,

wherein said forward vector unit candidate and said backward vector unit candidate are removed from the recombinant DNA base sequence [data], when there is only one candidate respectively for the specified forward and backward [vector units] base sequences, and the specified forward and backward [vector units] base sequences do not overlap each other.

39. (TWICE AMENDED)[The]A device [according to claim 38,] for analyzing base sequence data and removing, based on said data, a vector base sequence from a recombinant DNA base sequence, obtained as a result of performing a cloning process by integrating an object DNA fragment into a vector, comprising:

a database storing data identifying each of restriction enzymes, and data of base sequences at a plurality of restriction enzyme sites of a plurality of vectors correspondingly;

an obtaining unit obtaining base sequence data at a front restriction enzyme site and base sequence data at a back restriction enzyme site, as specified corresponding to a restriction enzyme used for cleaving the vector and a restriction enzyme used for obtaining the object DNA fragment, from the database;

a generation unit generating a first forward retrieval key using the obtained base sequence data of the front restriction enzyme site, and a first backward retrieval key using the obtained base sequence data of the back restriction enzyme site;

a retrieving unit retrieving base sequence data of the recombinant DNA

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obtained using the first forward and first backward retrieval keys, and specifying a junction between the vector and the object DNA fragment; and

a removal unit for removing the vector base sequence at the specified junction.

wherein each of said first forward and first backward retrieval keys includes sequence data including an end portion of the object DNA fragment and sequence data including an end portion of the vector base sequence, and specifies a candidate for the junction between the vector base sequence and the object DNA fragment.

wherein a second retrieval key, including sequence data longer than that of said first forward and first backward retrieval keys, is generated, and the junction is specified using the second retrieval key.

40. (TWICE AMENDED) The device according to Claim 39,

wherein said object DNA fragment is specified by removing the junction and base sequence [data] distal to the junction and the object DNA fragment from the DNA base sequence.